

## FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC  
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC  
GTTTGGCCCAGGACGGGGCCCATGTGGTTCGTACAGAGCCGGAAGCAGCAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA  
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC  
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC  
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA  
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT  
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTCTGC  
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTCTGCT  
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTCTGGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

FIGURE 1

## FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS  
SRKQQNVDDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG  
SIMDVTEEVWDKTLDIRVVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK  
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC  
AGIVSFLCSEDASYITGETVVVGGGTPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

1003344-12701

Figure 1 consists of 12 bar charts, labeled (a) through (l), each representing a different variable. Each chart compares the percentage of Clinton supporters (n=100) and Clinton opponents (n=100) for that variable. The y-axis for all charts represents the percentage of respondents, ranging from 0 to 100. The x-axis for each chart lists the categories for the variable.

- (a) Age:** Categories are 18-29, 30-39, 40-49, 50-59, 60-69, 70-79, 80-89, 90-99. Clinton supporters are generally older than opponents.
- (b) Sex:** Categories are Male, Female. Clinton supporters are slightly more female.
- (c) Education:** Categories are Less than high school, High school, Some college, College, Graduate school. Clinton supporters are more educated.
- (d) Income:** Categories are Less than \$10,000, \$10,000-\$19,999, \$20,000-\$29,999, \$30,000-\$39,999, \$40,000-\$49,999, \$50,000-\$59,999, \$60,000-\$69,999, \$70,000-\$79,999, \$80,000-\$89,999, \$90,000-\$99,999, \$100,000 or more. Clinton supporters have higher income.
- (e) Employment:** Categories are Not employed, Part-time, Full-time. Clinton supporters are more likely to be employed full-time.
- (f) Home ownership:** Categories are Own, Rent. Clinton supporters are more likely to own their home.
- (g) Marital status:** Categories are Single, Married, Divorced, Widowed. Clinton supporters are more likely to be married.
- (h) Political affiliation:** Categories are Democrat, Republican, Independent. Clinton supporters are more likely to be Democrats.
- (i) Party identification:** Categories are Democrat, Republican, Independent. Clinton supporters are more likely to identify with the Democratic Party.
- (j) Trust in Clinton:** Categories are No trust, Little trust, Some trust, A lot of trust. Clinton supporters have more trust in Clinton.
- (k) Confidence in Clinton:** Categories are No confidence, Little confidence, Some confidence, A lot of confidence. Clinton supporters have more confidence in Clinton.
- (l) Support for Clinton:** Categories are No support, Little support, Some support, A lot of support. Clinton supporters have more support for Clinton.

CGCGCCCTGAGCTCCGCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGCTCGAGGACCAGGCGGC  
CAGGGGGCCGCGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC  
GCGGCTGGAGGAGGAGAACCGAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC  
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGCGG  
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCCTCCCGGGTCCTTTGTGCCTCGACCTCATAC  
AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCTGCCTGCCTCCCTGGAGATG  
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGCCGCC  
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCAG  
GGAGTCTGCCAGAGAGGAAGGGCCCAGAGCTTTGCCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC  
AGAGCAGTTGGTGGGAGCAAGGCCCCAGTTCAGGCCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG  
GCGGCTGGCCAGGCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA  
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG  
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT  
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCGCGAGGAGGGTTCGCTG  
CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTTCG  
GCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA  
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC  
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA  
GAGATCGCGGCCCTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA  
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG  
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG  
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG  
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA  
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC  
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC  
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA  
CATGCCGCCAGCGGTGCTTCGGGCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC  
AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTGACAAGGTGGTGAC  
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCCTTCTCGGAACCTGGAGATGCAGCTGGAGGAGCAGC  
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC  
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA  
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACTGGGCCGTT  
ACATGTGGATAAACCAGGAACTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT  
GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC  
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT  
TGGTCCACGCTCCGTTACCCTTGACCTGGAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCCC  
GAGGAACTGAGGCAGCGGGAGGCGGCTGAGCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG  
CCTGCCCTGGAACCTTTGGGCCTTTGTCCAAGCCCCGGCGGGAACCTGCGACGAGCCAGCCCGGGGATGA  
TTGATGTCCGGAACAAACCCCTGTAAAGCCCTCGGGGCAGACCCTGCCCTTGAGGGGAGACTCCGAGCCT  
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCCTAAATCCAGG  
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCCCAAAGAACTGGACCCTCATTT  
AACAAAATAATATGCAATTTCCACCCTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCTTGTG  
TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTTACGGGGTTTG  
GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG  
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

## FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLELVPRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV  
LGMVPPACLPGLDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL  
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAAIPGSRAVGGSKARVQARQVPPATAS  
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE  
LERNVQLMRQQQGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQRRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS  
LRQEKDSSLKQRLEIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR  
ASASLLSQCEMNLMAKLSYLSSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG  
APRTREETRDVLHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

**Important features:**

**Leucine zipper pattern.**

amino acids 557-579, 794-815

**N-glycosylation sites.**

amino acids 133-136, 383-386

**Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

protein database

## FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCCTGTACCCATTAAAAACCCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

10/22/21 14:44:00

## FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSLWLCQPTPRCGNKIYNPSEQCCYDDAILS  
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRHVLYP

**Important features:**

**Signal sequence**

amino acids 1-21

**N-myristoylation sites.**

amino acids 33-39, 70-76

100344.1270

## FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT  
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG  
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG  
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT  
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCC  
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTAGTGGTCCGCCCCACGCGGG  
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCCGCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG  
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCTCGGCCGCGCTCCCCGCCCCGCC  
GCCCCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG  
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG  
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT  
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCCGGGGACAC  
CCCGCAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCGGAACCTCGCGCCCA  
CGCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG  
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT  
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA  
TCCACGTGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC  
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAA  
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCCATATGCCACTGTAC  
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC  
AAATGTAGACGCTTCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA  
CATTCTAGATGACTCTGGGAACCTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA  
TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT  
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG  
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAA  
AAAAAAAAAAAAAAAAAAAA

1023456789

## FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL  
GRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA  
AAAQDAIGPELAPTPEPPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL  
CAQPECPRHLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR  
IERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

TOGETHER



## FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTCAATCGGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTG  
CTACCTGTGTGAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT  
GAGCATTGAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGTTTGGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTACCGCTGCTGA  
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATCTACTCACCTAACAGCA  
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

1023456789

## FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRGRGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 243-260

**N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

**Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

**N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

TOGETHER

## FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG  
GCTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT  
TGTCGGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG  
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC  
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT  
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCCTGCGGCTCATCACCAAGTTCCAAGC  
ACCGCTGCATGGATAGCAGCGCCGCCTTCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC  
TTGCCCGCCCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT  
GAGATTTTTTGATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT  
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT  
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTACCTG  
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG  
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT  
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTTCAGCACTTGGACAAAGC  
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG  
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA  
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGC  
CTCGAACCTGATATTTGTGCTTTACCCTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC  
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCA  
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA  
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTATAGTAAGTGAAGAACATTTTT  
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATT  
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC  
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAA  
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCCTCCTAC  
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAAAGTGCT  
GGAGTAACAAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACTTTAC  
AGATTGTTCTGCAGTTCTCTCTTTCTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC  
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT  
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA  
TGAAAATAAATATTTTTGGTATTTTATTTATGAAATATTTGAACATTTTTTCAATAATTCTTT  
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCAATTCTGT  
CACTTGGCTTCGATTTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTTGTTTGATTT  
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA  
TAAAGAAAATTCTTGTGACTTTAAAAA

1022412241

## FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS  
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS  
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR  
CMDSSAAFLQGLWQHYPGLPPPVDADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH  
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA  
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE  
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV  
QMLLNEKVLPLAYSQETVSYEDLKNHYKDILQSCQTSEECELARANSTSDDEL

### **Important features:**

#### **Signal sequence**

amino acids 1-30

#### **N-glycosylation sites.**

amino acids 242-246, 481-485

#### **N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### **Endoplasmic reticulum targeting sequence.**

amino acids 484-489

TOGETHER

## FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGTTACAGGAATTTGAAAGTGTGGAACCTGTCTTGCATCATTACGGATTTCG  
AGACAAAGTGACCCCGAGATCGAGTGAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCCGAAGGAAATTTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCAGTGCCACGGATT  
CCAGAGCCAATCCCAGATTTTCGAATTTCTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTTGGGGGGGTTCTGGTTGTCTCTGCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCCACCTGGTCTGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAAAAACAACAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTGTGTTATTTTATAAAATTT  
TACATCTAAATTTTGTAAAGATGTATTTTGATTATTGAAAAAGAAATTTCTATTAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAATAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCCCTTTCT  
CACACAAGTTTTAGCCTTTTTTACAAAGGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGTCTCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCGCTGCGAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTGTTAATTATTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCACTGTTTCTCTTTGCCACAGAGAAAGCACCCAGAGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTATCCGCCGAGACACTGCTCCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA  
GAATGGCTCTCACTACTACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTC  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTAATAACACACCGTAATTTGGCATTTGTTTAA  
CTCATTTATAAAAGCTTCAAAAAACCCA

1003344.12701

## FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSKIIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

to get the

## FIGURE 15

CAGGACCAGGTCTTCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG  
ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG  
GAGAAGCCACTGCCCCACCGCTTCCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCCTGACTGGCTGAAGCTG  
CGCATGATCCGTTCTGAGGTGCTCCGCCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG  
TTCGTGCAGTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTTGGACCAGGCAGTGGCCAC  
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC  
GGCGCCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCGCCGAGACAGCACAGAGGCA  
CCCAAACCAAAGAGCAGCCAGAGCAGCCCATAGGCCAGGGCCGGATTCCGGTGGGGACCCAGCTCCGGGTGCTG  
GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCCGCTCAGCCCGGACCTCGGTGGCAGAGCTCC  
AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGCGCTCGTCCAGGGCAGCCCC  
GAGGTGCCGGGCATCACGGTGCCTGCTGCAGGCCCTCGCCACCCTGCTCAGCTCCCCACAGGCGGTGCCCTG  
GTGATGTCCATGCACCGTAGCCACTTCTGGCCTGCCCGCTGCTGCCAGCTCTGCCAGTACCAGCGCTGTGTG  
CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAGGTGCTCCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC  
GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCTCAGCCGGGCGCAGGCTCAGTGAT  
GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTCACTCCACCGTC  
CGTGCCGTGATCGCCACCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTTCCAG  
GGGCTGATCGAGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTGCTGCCACTGCGGATGCTGCC  
TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAAGTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG  
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCTCCTAGTGGACTGG  
CTGGAAATGCTGGACCCCGAGGTGGTCAAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG  
GGCAAAGGTCAAGCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCCTTTCACGCATCAGTCCAGCTGGCCC  
ACACTGCACCAGTGCATCCGAGTCCCTGCTGGGCAAGAGCCGGGAACAGAGGTTGACCCCTCTGCCTCTCTGGAC  
TTCCTCTGGGCCTGCATCCATGTTCTTCGCATCTGGCAGGGGCGGGACAGCGCACCCCGCAGAGCGGCGGAG  
GAGCTGGTGTGCGGGTCCAGGGCCCCGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG  
AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCAGGCCCGGCTGCCCTGCTCAGCTGCTGTGCTGTGGG  
GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA  
AGGCGCTGCCGAGACCTTCTCCTGCAGCTCTACCTACAGCGGCGGAGCTGCGGGTGGCCGTGCCTGAGGTCTTA  
CTGCACAGCGAAGGGGCTGCCAGCAGCAGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTCCTT  
GCGGACACCAGCGACTCCCGGGCGTTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG  
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCAGGCCCGCACCCACCTCAACTTC  
CAGGAGTTCGGGCAGCAGAACACCTGAGCTGCTTCTGCAGTGTGCGGCTGCTGGAGCTGCTGCAGCCGCAC  
GTGTTCCGAGCGAGCACCAGGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCTGCTGCTGAATTACAGG  
AAGTCTTCCCGCCATCTGGCTGCCTTCATCAACAAGTTTGTGCAAGTTCATCCATAAGTACATTACCTACAATGCC  
CCAGCAGCCATCTCCTTCTGCAGAAGCAGCCGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG  
ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGGACGACAGGACCGACCGAGGCTGGACGAAGAG  
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTCAGCGTCTCCTGTTCACCCCTCTGACCGCGGCGGAG  
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC  
GAGATGTCCCGCGGAGACCCGAGATCCTGAGCTTCTTCTGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG  
GAGTGTGCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGCAGCCGCTTTC  
CTGCCACGTTTCATGTACTGCTGGGCGAGCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG  
TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGCTTCTGGTGGGCATGTACGGCCAGATG  
GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA  
CCCCCTTCAAGCCCCGGCCCCGTCCCGTCCCCGGGGATCCTCGAGGCAAAGCCCAGGAAGCGTGGGCGTTGCTGG  
TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGAGGCCAGGAGCAATACTCCGAGCCCTGGGGTGG  
CTCCGGGCGGCGGCTGGCATCAGGGCCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCGG  
AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAAGTGTCAA

102344-102344

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRLM  
IRSEVLRLVDAALQDLEPQQLLLFVQSFQIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMHRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVLQMLQWLDSPG  
VEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ  
CSVEPDLISKVLQGLIEVRSPhLEELLTAFFSATADAASPFPAKPVVVVSSLLQEEEP  
GGKPGADGGSLEAVRLGPSSGLLDVLEMLDPEVVSSCPDLQLRLLFSRRKGKGAQVPSFR  
PYLLTLFTHQSSWPTLHQCIQIRVLLGKSREQRFDPSASLDLWACIHVPRIWQGRDQRT  
REELVLRVQGPPELISLVELILAEAEQSDGDTAACSLIQARLPLLLSCCCGDDES  
HLSGCIQQWGDVSLGRRCDLLQLYLQRPVPEVLLHSEGAASSSVCKLDGLIHRFI  
TLLADTSDSRALNRGADASMACRKLAVAHPLLLLRHLPMAALLHGRTHLNFQEF  
SCFLHVLGLLELLQPHVFRSEHQALWDCLLSFIRLLLNRYKSSRHAAAFINKFVQFI  
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGE  
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDEMSRRRPEILSFFST  
MSSAECCRNLAFLSLALRSMQNSPSIAAFLPTFMVCLGSQDFEVVQTALRNLPEYAL  
HAAVLLHRAFLVGMYGQMDPSAQISEALRIHMEAVM

**Important features:**

**Signal peptide:**

amino acids 1-16

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

**N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

**Amidation sites.**

amino acids 329-333, 634-638

104227-444



## FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGCTCCGC  
AATGGCACCTTCCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCCTCTCGCTGTCCTGGTA  
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCCTGGCGC  
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG  
GTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA  
TCGCACCTGGGGCCGCCTAACAGAGGACCCCGATTGAAGCCGTGGAACGGCTCACACCGGC  
ACGTGCTGCACCTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT  
CTGCAGCCCGCGGTGCGCGTGGGCCAGGGCCGCACCCGAGTGTGCGGTGGTGATGGGCATCCC  
GAGCGTGCAGCGCGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC  
TGAGCCCGCAGGAGAAGGAGGACTCGGTTCATCGTGGTGCTGATCGCCGAGACTGACTCACAG  
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT  
CCTGGAGGTCATCTCACCCCTCCCCCACTTCTACCCTGACTTCTCCCGCCTCCGAGAGTCCT  
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC  
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA  
GCCCAACTACCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA  
TCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG  
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT  
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA  
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT  
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT  
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAGCACTTCACCCTGGAGAAAG  
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC  
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGAGTGGAACATCGAGCACCC  
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACA  
AGGAGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC  
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC  
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCCTGTGTGGGTGATTCTGAGCGAGA  
TCTTCCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA  
GCCCACATTTCTGGGGGTGTGCTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCCAA  
AGGGTTCTGCCTGGCGTCGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCGGAGGCCCTA  
GGAGCTGGTGCTGCCCCCGCCCGCCGGGCCGCGGAGGAGGCAGGCGGCCCCCACACTGTGCC  
TGAGGCCCGGAACCGTTTCGCACCCGGCCTGCCCCAGTCAGGCCGTTTTAGAAAGAGCTTTTAC  
TTGGGCGCCCGCGTCTCTGGCGGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT  
TTTTATTCTTGATACATTTGATTTTTTTCAGTAAGTCCACATATACTTCTATAAGAGCGTG  
ACTTGTAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAA

Figure 17

## FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLTLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRLHAAEQESLKRSK  
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA  
KESSLQPAVRVGQGRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE  
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVVRWRTKQNLD  
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL  
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT  
HSSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD  
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS  
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

### **Important features:**

#### **Signal sequence**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

#### **N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515

10221-44220